

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/810,063A
Source: IFW16
Date Processed by STIC: 3/17/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/810,063A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220>
 → Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 03/17/2006

PATENT APPLICATION: US/10/810,063A

TIME: 14:03:30

Input Set : D:\INGN106.APP.txt

Output Set: N:\CRF4\03172006\J810063A.raw

3 <110> APPLICANT: WOLD, WILLIAM
 4 TOLLEFSON, ANN
 6 <120> TITLE OF INVENTION: ADENOVIRUS REPLICATION-COMPETENT VECTORS EXPRESSING
 7 TRAIL
 9 <130> FILE REFERENCE: INGN:106US
 11 <140> CURRENT APPLICATION NUMBER: 10/810,063A
 12 <141> CURRENT FILING DATE: 2004-03-26
 14 <150> PRIOR APPLICATION NUMBER: 60/458,493
 15 <151> PRIOR FILING DATE: 2003-03-28
 17 <160> NUMBER OF SEQ ID NOS: 3
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1769
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (88)..(933)
 30 <400> SEQUENCE: 1
 31 cctcactgac tataaaagaa tagagaagga agggcttcag tgaccggctg cctggctgac 60
 33 ttacagcagt cagactctga caggatc atg gct atg atg gag gtc cag ggg gga 114
 34 Met Ala Met Met Glu Val Gln Gly Gly
 35 1 5
 37 ccc agc ctg gga cag acc tgc gtg ctg atc gtg atc ttc aca gtg ctc 162
 38 Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val Leu
 39 10 15 20 25
 41 ctg cag tct ctc tgt gtg gct gta act tac gtg tac ttt acc aac gag 210
 42 Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn Glu
 43 30 35 40
 45 ctg aag cag atg cag gac aag tac tcc aaa agt ggc att gct tgt ttc 258
 46 Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe
 47 45 50 55
 49 tta aaa gaa gat gac agt tat tgg gac ccc aat gac gaa gag agt atg 306
 50 Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met
 51 60 65 70
 53 aac agc ccc tgc tgg caa gtc aag tgg caa ctc cgt cag ctc gtt aga 354
 54 Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val Arg
 55 75 80 85
 57 aag atg att ttg aga acc tct gag gaa acc att tct aca gtt caa gaa 402
 58 Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
 59 90 95 100 105
 61 aag caa caa aat att tct ccc cta gtg aga gaa aga ggt cct cag aga 450
 62 Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg

Does Not Comply
Corrected Diskette Needed

P.3

RAW SEQUENCE LISTING

DATE: 03/17/2006

PATENT APPLICATION: US/10/810,063A

TIME: 14:03:30

Input Set : D:\INGN106.APP.txt

Output Set: N:\CRF4\03172006\J810063A.raw

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63          110          115          120
65 gta gca gct cac ata act ggg acc aga gga aga agc aac aca ttg tct 498
66 Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
67          125          130          135
69 tct cca aac tcc aag aat gaa aag gct ctg ggc cgc aaa ata aac tcc 546
70 Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
71          140          145          150
73 tgg gaa tca tca agg agt ggg cat tca ttc ctg agc aac ttg cac ttg 594
74 Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
75          155          160          165
77 agg aat ggt gaa ctg gtc atc cat gaa aaa ggg ttt tac tac atc tat 642
78 Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
79 170          175          180          185
81 tcc caa aca tac ttt cga ttt cag gag gaa ata aaa gaa aac aca aag 690
82 Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
83          190          195          200
85 aac gac aaa caa atg gtc caa tat att tac aaa tac aca agt tat cct 738
86 Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
87          205          210          215
89 gac cct ata ttg ttg atg aaa agt gct aga aat agt tgt tgg tct aaa 786
90 Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
91          220          225          230
93 gat gca gaa tat gga ctc tat tcc atc tat caa ggg gga ata ttt gag 834
94 Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
95          235          240          245
97 ctt aag gaa aat gac aga att ttt gtt tct gta aca aat gag cac ttg 882
98 Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
99 250          255          260          265
101 ata gac atg gac cat gaa gcc agt ttt ttc ggg gcc ttt tta gtt ggc 930
102 Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
103          270          275          280
105 taa ctgacctgga aagaaaaagc aataacctca aagtgactat tcagttttca 983
108 ggatgataca ctatgaagat gtttcaaaaa atctgaccaa aacaaacaaa cagaaaacag 1043
110 aaaacaaaaa aacctctatg caatctgagt agagcagcca caacaaaaaa attctacaac 1103
112 acacactgtt ctgaaagtga ctcaactatc ccaagaaaat gaaattgctg aaagatcttt 1163
114 caggactcta cctcatatca gtttgctagc agaaatctag aagactgtca gcttccaaac 1223
116 attaatgcaa tgggtaacat cttctgtctt tataatctac tccttgtaaa gactgtagaa 1283
118 gaaagcgcaa caatccatct ctcaagtagt gtatcacagt agtagcctcc aggtttcctt 1343
120 aagggacaac atccttaagt caaaagagag aagaggcacc actaaaagat cgcagtttgc 1403
122 ctggtgcagt ggctcacacc tgtaatccca acattttggg aacccaaggt gggtagatca 1463
124 cgagatcaag agatcaagac catagtgacc aacatagtga aaccccatct ctactgaaag 1523
126 tgcaaaaatt agctgggtgt gttggcacat gcctgtagtc ccagctactt gagaggctga 1583
128 ggcaggagaa tcgtttgaac ccgggaggca gagggtgcag tgtggtgaga tcatgccact 1643
130 acactccagc ctggcgacag agcgagactt gggtttcaaaa aaaaaaaaaa aaaaaaactt 1703
132 cagtaagtac gtgttatttt tttcaataaa attctattac agtatgtcaa aaaaaaaaaa 1763
134 aaaaaa 1769
137 <210> SEQ ID NO: 2
138 <211> LENGTH: 281
139 <212> TYPE: PRT

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RAW SEQUENCE LISTING

DATE: 03/17/2006

PATENT APPLICATION: US/10/810,063A

TIME: 14:03:30

Input Set : D:\INGN106.APP.txt

Output Set: N:\CRF4\03172006\J810063A.raw

140 <213> ORGANISM: Homo sapiens
 142 <400> SEQUENCE: 2
 143 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
 144 1 5 10 15
 145 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
 146 20 25 30
 147 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
 148 35 40 45
 149 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
 150 50 55 60
 151 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
 152 65 70 75 80
 153 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
 154 85 90 95
 155 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
 156 100 105 110
 157 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
 158 115 120 125
 159 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
 160 130 135 140
 161 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
 162 145 150 155 160
 163 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
 164 165 170 175
 165 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
 166 180 185 190
 167 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
 168 195 200 205
 169 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
 170 210 215 220
 171 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
 172 225 230 235 240
 173 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
 174 245 250 255
 175 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 176 260 265 270
 177 Ser Phe Phe Gly Ala Phe Leu Val Gly
 178 275 280
 182 <210> SEQ ID NO: 3
 183 <211> LENGTH: 14
 184 <212> TYPE: DNA
 185 <213> ORGANISM: Artificial Sequence
 187 <220> FEATURE:
 188 <221> NAME/KEY: modified base
 189 <222> LOCATION: (3)..(12)
 190 <223> OTHER INFORMATION: n = a, c, g and/or t/u
 192 <400> SEQUENCE: 3
 W--> 193 ctngaannatt cnag

*Needs exploration
 (see item 11 on Euro
 summary
 sheet)*

14

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/17/2006
PATENT APPLICATION: US/10/810,063A TIME: 14:03:31

Input Set : D:\INGN106.APP.txt
Output Set: N:\CRF4\03172006\J810063A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,7,8,12

VERIFICATION SUMMARY

DATE: 03/17/2006

PATENT APPLICATION: US/10/810,063A

TIME: 14:03:31

Input Set : D:\INGN106.APP.txt

Output Set: N:\CRF4\03172006\J810063A.raw

L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0